

## SEQUENCE LISTING

<110> Presnell, Scott R.  
Burkhead, Steven K.  
Powder, Sarah L.

<120> Human Cytokine Receptor

<130> 99-50

<160> 12

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 2255

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (154)...(2229)

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cctcaggcct gggtgccacc tggcacctag aag atg cct gtg ccc tgg ttc ttg 174  
Met Pro Val Pro Trp Phe Leu  
1 5

ctg tcc ttg gca ctg ggc cga agc cca gtg gtc ctt tct ctg gag agg 222  
Leu Ser Leu Ala Leu Gly Arg Ser Pro Val Val Leu Ser Leu Glu Arg  
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ctt gtg ggg cct cag gac gct acc cac tgc tct ccg ggc ctc tcc tgc 270  
Leu Val Gly Pro Gln Asp Ala Thr His Cys Ser Pro Gly Leu Ser Cys  
25 30 35

cgc ctc tgg gac agt gac ata ctc tgc ctg cct ggg gac atc gtg cct 318  
Arg Leu Trp Asp Ser Asp Ile Leu Cys Leu Pro Gly Asp Ile Val Pro  
40 45 50 55

Sub A1

A

[illegible]

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235 240 245	
aac cac aca gac ctg gtt ccc tgc ctc tgt att cag gtg tgg cct ctg	942
Asn His Thr Asp Leu Val Pro Cys Leu Cys Ile Gln Val Trp Pro Leu	
250 255 260	
gaa cct gac tcc gtt agg acg aac atc tgc ccc ttc agg gag gac ccc	990
Glu Pro Asp Ser Val Arg Thr Asn Ile Cys Pro Phe Arg Glu Asp Pro	
265 270 275	
cgc gca cac cag aac ctc tgg caa gcc gcc cga ctg cga ctg ctg acc	1038
Arg Ala His Gln Asn Leu Trp Gln Ala Ala Arg Leu Arg Leu Leu Thr	
280 285 290 295	
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Leu Gln Ser Trp Leu Leu Asp Ala Pro Cys Ser Leu Pro Ala Glu Ala	
300 305 310	
gca ctg tgc tgg cgg gct ccg ggt ggg gac ccc tgc cag cca ctg gtc	1134
Ala Leu Cys Trp Arg Ala Pro Gly Gly Asp Pro Cys Gln Pro Leu Val	
315 320 325	
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Pro Pro Leu Ser Trp Glu Asn Val Thr Val Asp Lys Val Leu Glu Phe	
330 335 340	
cca ttg ctg aaa ggc cac cct aac ctc tgt gtt cag gtg aac agc tcg	1230
Pro Leu Leu Lys Gly His Pro Asn Leu Cys Val Gln Val Asn Ser Ser	
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Glu Lys Leu Gln Leu Gln Glu Cys Leu Trp Ala Asp Ser Leu Gly Pro	
360 365 370 375	
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Leu Lys Asp Asp Val Leu Leu Leu Glu Thr Arg Gly Pro Gln Asp Asn	
380 385 390	
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Arg Ser Leu Cys Ala Leu Glu Pro Ser Gly Cys Thr Ser Leu Pro Ser	
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Lys Ala Ser Thr Arg Ala Ala Arg Leu Gly Glu Tyr Leu Leu Gln Asp	
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Val Trp Leu Ala Cys Leu Leu Phe Ala Ala Ala Leu Ser Leu Ile Leu	
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475 480 485	
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Leu Leu Leu Tyr Ser Ala Asp Asp Ser Gly Phe Glu Arg Leu Val Gly	
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His Ala Gln Arg Arg Gln Thr Leu Gln Glu Gly Gly Val Val Val Leu	
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Met Pro Val Pro Trp Phe Leu Leu Ser Leu Ala Leu Gly Arg Ser Pro  
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Leu	Pro	Gly	Asp	Ile	Val	Pro	Ala	Pro	Gly	Pro	Val	Leu	Ala	Pro	Thr
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Val	Glu	Glu	Pro	Arg	Asn	Ala	Ser	Leu	Gln	Ala	Gln	Val	Val	Leu	Ser
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Asp	Cys	Phe	Glu	Ala	Ala	Leu	Gly	Ser	Glu	Val	Arg	Ile	Trp	Ser	Tyr
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Thr	Gln	Pro	Arg	Tyr	Glu	Lys	Glu	Leu	Asn	His	Thr	Gln	Gln	Leu	Pro
			180					185					190		
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Asn	Gln	Val	Gln	Gly	Pro	Pro	Lys	Pro	Arg	Trp	His	Lys	Asn	Leu	Thr
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Gly	Pro	Gln	Ile	Ile	Thr	Leu	Asn	His	Thr	Asp	Leu	Val	Pro	Cys	Leu
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Cys	Ile	Gln	Val	Trp	Pro	Leu	Glu	Pro	Asp	Ser	Val	Arg	Thr	Asn	Ile
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Cys	Pro	Phe	Arg	Glu	Asp	Pro	Arg	Ala	His	Gln	Asn	Leu	Trp	Gln	Ala
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Asp	Pro	Cys	Gln	Pro	Leu	Val	Pro	Pro	Leu	Ser	Trp	Glu	Asn	Val	Thr
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 370 375 380  
 Thr Arg Gly Pro Gln Asp Asn Arg Ser Leu Cys Ala Leu Glu Pro Ser  
 385 390 395 400  
 Gly Cys Thr Ser Leu Pro Ser Lys Ala Ser Thr Arg Ala Ala Arg Leu  
 405 410 415  
 Gly Glu Tyr Leu Leu Gln Asp Leu Gln Ser Gly Gln Cys Leu Gln Leu  
 420 425 430  
 Trp Asp Asp Asp Leu Gly Ala Leu Trp Ala Cys Pro Met Asp Lys Tyr  
 435 440 445  
 Ile His Lys Arg Trp Ala Leu Val Trp Leu Ala Cys Leu Leu Phe Ala  
 450 455 460  
 Ala Ala Leu Ser Leu Ile Leu Leu Lys Lys Asp His Ala Lys Ala  
 465 470 475 480  
 Ala Ala Arg Gly Arg Ala Ala Leu Leu Leu Tyr Ser Ala Asp Asp Ser  
 485 490 495  
 Gly Phe Glu Arg Leu Val Gly Ala Leu Ala Ser Ala Leu Cys Gln Leu  
 500 505 510  
 Pro Leu Arg Val Ala Val Asp Leu Trp Ser Arg Arg Glu Leu Ser Ala  
 515 520 525  
 Gln Gly Pro Val Ala Trp Phe His Ala Gln Arg Arg Gln Thr Leu Gln  
 530 535 540  
 Glu Gly Gly Val Val Val Leu Leu Phe Ser Pro Gly Ala Val Ala Leu  
 545 550 555 560  
 Cys Ser Glu Trp Leu Gln Asp Gly Val Ser Gly Pro Gly Ala His Gly  
 565 570 575  
 Pro His Asp Ala Phe Arg Ala Ser Leu Ser Cys Val Leu Pro Asp Phe  
 580 585 590  
 Leu Gln Gly Arg Ala Pro Gly Ser Tyr Val Gly Ala Cys Phe Asp Arg  
 595 600 605  
 Leu Leu His Pro Asp Ala Val Pro Ala Leu Phe Arg Thr Val Pro Val  
 610 615 620  
 Phe Thr Leu Pro Ser Gln Leu Pro Asp Phe Leu Gly Ala Leu Gln Gln  
 625 630 635 640  
 Pro Arg Ala Pro Arg Ser Gly Arg Leu Gln Glu Arg Ala Glu Gln Val  
 645 650 655  
 Ser Arg Ala Leu Gln Pro Ala Leu Asp Ser Tyr Phe His Pro Pro Gly  
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Gly Asp Gly Thr  
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<210> 3

<211> 2076

<212> DNA

<213> Artificial Sequence

<220>

<223> This degenerate sequence encodes the amino acid  
sequence of SEQ ID NO:2.

<221> variation

<222> (1)...(2076)

<223> N is any nucleotide

<221> misc\_feature

<222> (1)...(2076)

<223> n = A,T,C or G

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ytngcncna	cncayytnc	racngarytn	gtnytnmgnt	gycaraarga	racngaytgy	240
gayytntggy	tnmgngtngc	ngtncayytn	gcngtncayg	gncaytggga	rgarccngar	300
gaygargara	arttyggngg	ngcngcngay	wsngngtng	argarccnmg	naaygcnwsn	360
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gargtncarg	tnccngcngc	nytngtncar	ttyggncarw	sngtnggnws	ngtngtntay	480
gaytgyttyg	argcngcnyt	nggnwsngar	gtnmgnatht	ggwsntayac	ncarccnmgn	540
taygaraarg	arytnaayca	yacncarcar	ytncngcny	tnccntggyt	naaygtnwsn	600
gcngayggng	ayaaygtnc	yytngtynytn	aaygtnwsng	argarcarca	yttyggnytn	660
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gcncaycara	ayytntggca	rgcngcnmgn	ytngmnytny	tnacnytnca	rwsntggytn	900
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gayccntgyc	arccnytngt	nccncnytn	wsntgggara	aygtnacngt	ngayaargtn	1020
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acngtnccng	tnntyacny	nccnwsncar	ytncngayt	tytnggngc	nytnccar	1920
ccnmngcnc	cnmgngwsngg	nmgnytnar	garmgngcng	arcargtnws	nmgngcnytn	1980
carccngcny	tngaywsnta	ytycayccn	ccnggnacnc	cngcncngg	nmgnggngtn	2040
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&lt;210&gt; 4

&lt;211&gt; 1753

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (2)...(1726)

&lt;400&gt; 4

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cag	gcc	tac	cct	act	gcc	cgc	tgc	gtc	ctg	ctg	gag	gtg	caa	gtg	cct	97
Gln	Ala	Tyr	Pro	Thr	Ala	Arg	Cys	Val	Leu	Leu	Glu	Val	Gln	Val	Pro	
			20					25					30			

gct	gcc	ctt	gtg	cag	ttt	ggt	cag	tct	gtg	ggc	tct	gtg	gta	tat	gac	145
Ala	Ala	Leu	Val	Gln	Phe	Gly	Gln	Ser	Val	Gly	Ser	Val	Val	Tyr	Asp	
		35					40					45				

tgc	ttc	gag	gct	gcc	cta	ggg	agt	gag	gta	cga	atc	tgg	tcc	tat	act	193
Cys	Phe	Glu	Ala	Ala	Leu	Gly	Ser	Glu	Val	Arg	Ile	Trp	Ser	Tyr	Thr	
	50					55				60						

cag	ccc	agg	tac	gag	aag	gaa	ctc	aac	cac	aca	cag	cag	ctg	cct	gcc	241
Gln	Pro	Arg	Tyr	Glu	Lys	Glu	Leu	Asn	His	Thr	Gln	Gln	Leu	Pro	Ala	
	65					70				75					80	

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Leu Pro Trp Leu Asn Val Ser Ala Asp Gly Asp Asn Val His Leu Val	
85 90 95	
ctg aat gtc tct gag gag cag cac ttc ggc ctc tcc ctg tac tgg aat	337
Leu Asn Val Ser Glu Glu Gln His Phe Gly Leu Ser Leu Tyr Trp Asn	
100 105 110	
cag gtc cag ggc ccc cca aaa ccc cgg tgg cac aaa aac ctg act gga	385
Gln Val Gln Gly Pro Pro Lys Pro Arg Trp His Lys Asn Leu Thr Gly	
115 120 125	
ccg cag atc att acc ttg aac cac aca gac ctg gtt ccc tgc ctc tgt	433
Pro Gln Ile Ile Thr Leu Asn His Thr Asp Leu Val Pro Cys Leu Cys	
130 135 140	
att cag gtg tgg cct ctg gaa cct gac tcc gtt agg acg aac atc tgc	481
Ile Gln Val Trp Pro Leu Glu Pro Asp Ser Val Arg Thr Asn Ile Cys	
145 150 155 160	
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Pro Phe Arg Glu Asp Pro Arg Ala His Gln Asn Leu Trp Gln Ala Ala	
165 170 175	
cga ctg cga ctg ctg acc ctg cag agc tgg ctg ctg gac gca ccg tgc	577
Arg Leu Arg Leu Leu Thr Leu Gln Ser Trp Leu Leu Asp Ala Pro Cys	
180 185 190	
tcg ctg ccc gca gaa gcg gca ctg tgc tgg cgg gct ccg ggt ggg gac	625
Ser Leu Pro Ala Glu Ala Ala Leu Cys Trp Arg Ala Pro Gly Gly Asp	
195 200 205	
ccc tgc cag cca ctg gtc cca ccg ctt tcc tgg gag aac gtc act gtg	673
Pro Cys Gln Pro Leu Val Pro Pro Leu Ser Trp Glu Asn Val Thr Val	
210 215 220	
gac gtg aac agc tcg gag aag ctg cag ctg cag gag tgc ttg tgg gct	721
Asp Val Asn Ser Ser Glu Lys Leu Gln Leu Gln Glu Cys Leu Trp Ala	
225 230 235 240	
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Asp	Ser	Leu	Gly	Pro	Leu	Lys	Asp	Asp	Val	Leu	Leu	Leu	Glu	Thr	Arg	
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Gly	Pro	Gln	Asp	Asn	Arg	Ser	Leu	Cys	Ala	Leu	Glu	Pro	Ser	Gly	Cys	
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act	tca	cta	ccc	agc	aaa	gcc	tcc	acg	agg	gca	gct	cgc	ctt	gga	gag	865
Thr	Ser	Leu	Pro	Ser	Lys	Ala	Ser	Thr	Arg	Ala	Ala	Arg	Leu	Gly	Glu	
		275					280					285				
tac	tta	cta	caa	gac	ctg	cag	tca	ggc	cag	tgt	ctg	cag	cta	tgg	gac	913
Tyr	Leu	Leu	Gln	Asp	Leu	Gln	Ser	Gly	Gln	Cys	Leu	Gln	Leu	Trp	Asp	
	290					295					300					
gat	gac	ttg	gga	gcg	cta	tgg	gcc	tgc	ccc	atg	gac	aaa	tac	atc	cac	961
Asp	Asp	Leu	Gly	Ala	Leu	Trp	Ala	Cys	Pro	Met	Asp	Lys	Tyr	Ile	His	
305					310					315					320	
aag	cgc	tgg	gcc	ctc	gtg	tgg	ctg	gcc	tgc	cta	ctc	ttt	gcc	gct	gcg	1009
Lys	Arg	Trp	Ala	Leu	Val	Trp	Leu	Ala	Cys	Leu	Leu	Phe	Ala	Ala	Ala	
				325					330					335		
ctt	tcc	ctc	atc	ctc	ctt	ctc	aaa	aag	gat	cac	gcg	aaa	ggg	tgg	ctg	1057
Leu	Ser	Leu	Ile	Leu	Leu	Leu	Lys	Lys	Asp	His	Ala	Lys	Gly	Trp	Leu	
			340					345					350			
agg	ctc	ttg	aaa	cag	gac	gtc	cgc	tcg	ggg	gcg	gcc	gcc	agg	ggc	cgc	1105
Arg	Leu	Leu	Lys	Gln	Asp	Val	Arg	Ser	Gly	Ala	Ala	Ala	Arg	Gly	Arg	
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gcg	gct	ctg	ctc	ctc	tac	tca	gcc	gat	gac	tcg	ggt	ttc	gag	cgc	ctg	1153
Ala	Ala	Leu	Leu	Leu	Tyr	Ser	Ala	Asp	Asp	Ser	Gly	Phe	Glu	Arg	Leu	
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Val	Gly	Ala	Leu	Ala	Ser	Ala	Leu	Cys	Gln	Leu	Pro	Leu	Arg	Val	Ala	
385					390					395					400	
gta	gac	ctg	tgg	agc	cgt	cgt	gaa	ctg	agc	gcg	cag	ggg	ccc	gtg	gct	1249
Val	Asp	Leu	Trp	Ser	Arg	Arg	Glu	Leu	Ser	Ala	Gln	Gly	Pro	Val	Ala	
				405					410					415		

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Trp Phe His Ala Gln Arg Arg Gln Thr Leu Gln Glu Gly Gly Val Val	
420 425 430	
gtc ttg ctc ttc tct ccc ggt gcg gtg gcg ctg tgc agc gag tgg cta	1345
Val Leu Leu Phe Ser Pro Gly Ala Val Ala Leu Cys Ser Glu Trp Leu	
435 440 445	
cag gat ggg gtg tcc ggg ccc ggg gcg cac ggc ccg cac gac gcc ttc	1393
Gln Asp Gly Val Ser Gly Pro Gly Ala His Gly Pro His Asp Ala Phe	
450 455 460	
cgc gcc tcg ctc agc tgc gtg ctg ccc gac ttc ttg cag ggc cgg gcg	1441
Arg Ala Ser Leu Ser Cys Val Leu Pro Asp Phe Leu Gln Gly Arg Ala	
465 470 475 480	
ccc ggc agc tac gtg ggg gcc tgc ttc gac agg ctg ctc cac ccg gac	1489
Pro Gly Ser Tyr Val Gly Ala Cys Phe Asp Arg Leu Leu His Pro Asp	
485 490 495	
gcc gta ccc gcc ctt ttc cgc acc gtg ccc gtc ttc aca ctg ccc tcc	1537
Ala Val Pro Ala Leu Phe Arg Thr Val Pro Val Phe Thr Leu Pro Ser	
500 505 510	
caa ctg cca gac ttc ctg ggg gcc ctg cag cag cct cgc gcc ccg cgt	1585
Gln Leu Pro Asp Phe Leu Gly Ala Leu Gln Gln Pro Arg Ala Pro Arg	
515 520 525	
tcc ggg cgg ctc caa gag aga gcg gag caa gtg tcc cgg gcc ctt cag	1633
Ser Gly Arg Leu Gln Glu Arg Ala Glu Gln Val Ser Arg Ala Leu Gln	
530 535 540	
cca gcc ctg gat agc tac ttc cat ccc ccg ggg act ccc gcg ccg gga	1681
Pro Ala Leu Asp Ser Tyr Phe His Pro Pro Gly Thr Pro Ala Pro Gly	
545 550 555 560	
cgc ggg gtg gga cca ggg gcg gga cct ggg gcg ggg gac ggg act	1726
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 <213> Homo sapiens

<400> 5

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		180						185					190		
Ser	Leu	Pro	Ala	Glu	Ala	Ala	Leu	Cys	Trp	Arg	Ala	Pro	Gly	Gly	Asp
		195					200					205			
Pro	Cys	Gln	Pro	Leu	Val	Pro	Pro	Leu	Ser	Trp	Glu	Asn	Val	Thr	Val
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		260						265					270		
Thr	Ser	Leu	Pro	Ser	Lys	Ala	Ser	Thr	Arg	Ala	Ala	Arg	Leu	Gly	Glu
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Tyr	Leu	Leu	Gln	Asp	Leu	Gln	Ser	Gly	Gln	Cys	Leu	Gln	Leu	Trp	Asp
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Asp Asp Leu Gly Ala Leu Trp Ala Cys Pro Met Asp Lys Tyr Ile His
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Lys Arg Trp Ala Leu Val Trp Leu Ala Cys Leu Leu Phe Ala Ala Ala
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Gln Asp Gly Val Ser Gly Pro Gly Ala His Gly Pro His Asp Ala Phe
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Arg Ala Ser Leu Ser Cys Val Leu Pro Asp Phe Leu Gln Gly Arg Ala
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<211> 1725

<212> DNA

<213> Artificial Sequence

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<223> This degenerate sequence encodes the amino acid  
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 <222> (1)...(1725)  
 <223> N is any nucleotide.

<221> misc\_feature  
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 <223> n = A,T,C or G

<400> 6

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tggwsntaya	cncarcnmg	ntaygaraar	garytnaayc	ayacncarca	rytnccngcn	240
ytnccntggy	tnaaygtwsw	ngcngayggn	gayaaygtnc	ayytngtny	naaygtwsw	300
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 Leu Pro Gly Asp Ile Val Pro Ala Pro Gly Pro Val Leu Ala Pro Thr  
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 His Leu Gln Thr Glu Leu Val Leu Arg Cys Gln Lys Glu Thr Asp Cys  
 65 70 75 80  
 Asp Leu Cys Leu Arg Val Ala Val His Leu Ala Val His Gly His Trp  
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 Glu Glu Pro Glu Asp Glu Glu Lys Phe Gly Gly Ala Ala Asp Ser Gly  
 100 105 110  
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 Phe Gln Ala Tyr Pro Thr Ala Arg Cys Val Leu Leu Glu Val Gln Val  
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 Pro Ala Ala Leu Val Gln Phe Gly Gln Ser Val Gly Ser Val Val Tyr  
 145 150 155 160  
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 165 170 175  
 Thr Gln Pro Arg Tyr Glu Lys Glu Leu Asn His Thr Gln Gln Leu Pro  
 180 185 190  
 Ala Leu Pro Trp Leu Asn Val Ser Ala Asp Gly Asp Asn Val His Leu  
 195 200 205  
 Val Leu Asn Val Ser Glu Glu Gln His Phe Gly Leu Ser Leu Tyr Trp  
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 225 230 235 240  
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 Cys Ile Gln Val Trp Pro Leu Glu Pro Asp Ser Val Arg Thr Asn Ile  
 260 265 270  
 Cys Pro Phe Arg Glu Asp Pro Arg Ala His Gln Asn Leu Trp Gln Ala  
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 Cys Ser Leu Pro Ala Glu Ala Ala Leu Cys Trp Arg Ala Pro Gly Gly  
 305 310 315 320  
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Ala Asp Ser Leu Gly Pro Leu Lys Asp Asp Val Leu Leu Leu Glu Thr  
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 Arg Gly Pro Gln Asp Asn Arg Ser Leu Cys Ala Leu Glu Pro Ser Gly  
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 His Lys Arg Trp Ala Leu Val Trp Leu Ala Cys Leu Leu Phe Ala Ala  
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 465 470 475 480  
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 Ala Val Asp Leu Trp Ser Arg Arg Glu Leu Ser Ala Gln Gly Pro Val  
 515 520 525  
 Ala Trp Phe His Ala Gln Arg Arg Gln Thr Leu Gln Glu Gly Gly Val  
 530 535 540  
 Val Val Leu Leu Phe Ser Pro Gly Ala Val Ala Leu Cys Ser Glu Trp  
 545 550 555 560  
 Leu Gln Asp Gly Val Ser Gly Pro Gly Ala His Gly Pro His Asp Ala  
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 Ala Pro Gly Ser Tyr Val Gly Ala Cys Phe Asp Arg Leu Leu His Pro  
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 Ser Gln Leu Pro Asp Phe Leu Gly Ala Leu Gln Gln Pro Arg Ala Pro  
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 Arg Ser Gly Arg Leu Gln Glu Arg Ala Glu Gln Val Ser Arg Ala Leu  
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 35 40 45  
 Leu Pro Gly Asp Ile Val Pro Ala Pro Gly Pro Val Leu Ala Pro Thr  
 50 55 60  
 His Leu Gln Thr Glu Leu Val Leu Arg Cys Gln Lys Glu Thr Asp Cys  
 65 70 75 80  
 Asp Leu Cys Leu Arg Val Ala Val His Leu Ala Val His Gly His Trp  
 85 90 95  
 Glu Glu Pro Glu Asp Glu Glu Lys Phe Gly Gly Ala Ala Asp Ser Gly  
 100 105 110  
 Val Glu Glu Pro Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu Ser  
 115 120 125  
 Phe Gln Ala Tyr Pro Thr Ala Arg Cys Val Leu Leu Glu Val Gln Val  
 130 135 140  
 Pro Ala Ala Leu Val Gln Phe Gly Gln Ser Val Gly Ser Val Val Tyr  
 145 150 155 160  
 Asp Cys Phe Glu Ala Ala Leu Gly Ser Glu Val Arg Ile Trp Ser Tyr  
 165 170 175  
 Thr Gln Pro Arg Tyr Glu Lys Glu Leu Asn His Thr Gln Gln Leu Pro  
 180 185 190  
 Ala Leu Pro Trp Leu Asn Val Ser Ala Asp Gly Asp Asn Val His Leu  
 195 200 205  
 Val Leu Asn Val Ser Glu Glu Gln His Phe Gly Leu Ser Leu Tyr Trp  
 210 215 220  
 Asn Gln Val Gln Gly Pro Pro Lys Pro Arg Trp His Lys Asn Leu Thr  
 225 230 235 240  
 Gly Pro Gln Ile Ile Thr Leu Asn His Thr Asp Leu Val Pro Cys Leu  
 245 250 255  
 Cys Ile Gln Val Trp Pro Leu Glu Pro Asp Ser Val Arg Thr Asn Ile  
 260 265 270

Sub A1  
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Cys Pro Phe Arg Glu Asp Pro Arg Ala His Gln Asn Leu Trp Gln Ala  
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 Ala Arg Leu Arg Leu Leu Thr Leu Gln Ser Trp Leu Leu Asp Ala Pro  
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 Cys Ser Leu Pro Ala Glu Ala Ala Leu Cys Trp Arg Ala Pro Gly Gly  
 305 310 315 320  
 Asp Pro Cys Gln Pro Leu Val Pro Pro Leu Ser Trp Glu Asn Val Thr  
 325 330 335  
 Val Asp Lys Val Leu Glu Phe Pro Leu Leu Lys Gly His Pro Asn Leu  
 340 345 350  
 Cys Val Gln Val Asn Ser Ser Glu Lys Leu Gln Leu Gln Glu Cys Leu  
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 Trp Ala Asp Ser Leu Gly Pro Leu Lys Asp Asp Val Leu Leu Leu Glu  
 370 375 380  
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 Gly Cys Thr Ser Leu Pro Ser Lys Ala Ser Thr Arg Ala Ala Arg Leu  
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 Trp Asp Asp Asp Leu Gly Ala Leu Trp Ala Cys Pro Met Asp Lys Tyr  
 435 440 445  
 Ile His Lys Arg Trp Ala Leu Val Trp Leu Ala Cys Leu Leu Phe Ala  
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 565 570 575  
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Sub A1  
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 645 650 655  
 Pro Arg Ser Gly Arg Leu Gln Glu Arg Ala Glu Gln Val Ser Arg Ala  
 660 665 670  
 Leu Gln Pro Ala Leu Asp Ser Tyr Phe His Pro Pro Gly Thr Pro Ala  
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 Thr  
 705

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<400> 12

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 50 55 60  
 His Leu Gln Thr Glu Leu Val Leu Arg Cys Gln Lys Glu Thr Asp Cys  
 65 70 75 80  
 Asp Leu Cys Leu Arg Val Ala Val His Leu Ala Val His Gly His Trp  
 85 90 95  
 Glu Glu Pro Glu Asp Glu Glu Lys Phe Gly Gly Ala Ala Asp Ser Gly  
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 Val Glu Glu Pro Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu Ser  
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 Phe Gln Ala Tyr Pro Thr Ala Arg Cys Val Leu Leu Glu Val Gln Val  
 130 135 140

SubA  
Cont.

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 Ala Leu Pro Trp Leu Asn Val Ser Ala Asp Gly Asp Asn Val His Leu  
 195 200 205  
 Val Leu Asn Val Ser Glu Glu Gln His Phe Gly Leu Ser Leu Tyr Trp  
 210 215 220  
 Asn Gln Val Gln Gly Pro Pro Lys Pro Arg Trp His Lys Asn Leu Thr  
 225 230 235 240  
 Gly Pro Gln Ile Ile Thr Leu Asn His Thr Asp Leu Val Pro Cys Leu  
 245 250 255  
 Cys Ile Gln Val Trp Pro Leu Glu Pro Asp Ser Val Arg Thr Asn Ile  
 260 265 270  
 Cys Pro Phe Arg Glu Asp Pro Arg Ala His Gln Asn Leu Trp Gln Ala  
 275 280 285  
 Ala Arg Leu Arg Leu Leu Thr Leu Gln Ser Trp Leu Leu Asp Ala Pro  
 290 295 300  
 Cys Ser Leu Pro Ala Glu Ala Ala Leu Cys Trp Arg Ala Pro Gly Gly  
 305 310 315 320  
 Asp Pro Cys Gln Pro Leu Val Pro Pro Leu Ser Trp Glu Asn Val Thr  
 325 330 335  
 Val Asp Val Asn Ser Ser Glu Lys Leu Gln Leu Gln Glu Cys Leu Trp  
 340 345 350  
 Ala Asp Ser Leu Gly Pro Leu Lys Asp Asp Val Leu Leu Glu Thr  
 355 360 365  
 Arg Gly Pro Gln Asp Asn Arg Ser Leu Cys Ala Leu Glu Pro Ser Gly  
 370 375 380  
 Cys Thr Ser Leu Pro Ser Lys Ala Ser Thr Arg Ala Ala Arg Leu Gly  
 385 390 395 400  
 Glu Tyr Leu Leu Gln Asp Leu Gln Ser Gly Gln Cys Leu Gln Leu Trp  
 405 410 415  
 Asp Asp Asp Leu Gly Ala Leu Trp Ala Cys Pro Met Asp Lys Tyr Ile  
 420 425 430  
 His Lys Arg Trp Ala Leu Val Trp Leu Ala Cys Leu Leu Phe Ala Ala  
 435 440 445  
 Ala Leu Ser Leu Ile Leu Leu Leu Lys Lys Asp His Ala Lys Ala Ala  
 450 455 460  
 Ala Arg Gly Arg Ala Ala Leu Leu Leu Tyr Ser Ala Asp Asp Ser Gly  
 465 470 475 480

Sub A  
cont.

145 150 155 160  
 165 170 175  
 180 185 190  
 195 200 205  
 210 215 220  
 225 230 235 240  
 245 250 255  
 260 265 270  
 275 280 285  
 290 295 300  
 305 310 315 320  
 325 330 335  
 340 345 350  
 355 360 365  
 370 375 380  
 385 390 395 400  
 405 410 415  
 420 425 430  
 435 440 445  
 450 455 460  
 465 470 475 480

Sub A  
cont.